



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 144275

To: Nita M Minnifield  
Location: REM 3C01/3C18  
Art Unit: 1645  
Friday, February 04, 2005

Case Serial Number: 09/837344

From: Beverly Shears  
Location: Remsen Bldg.  
RM 1A54  
Phone: 571-272-2528

beverly.shears@uspto.gov

### Search Notes

*Reviewed  
2/7/05*

Shears, Beverly

144275

From: Minnifield, Nita 71976  
Sent: Thursday, February 03, 2005 11:21 AM  
To: Shears, Beverly  
Subject: RE: sequence search request

09/837344

Beverly,  
I checked the complete RSL and the previous search report, could you search SEQ ID NO: 31 and 20 (both aa) on commercial and interference databases.

Thanks,  
Nita

-----Original Message-----

From: Shears, Beverly  
Sent: Wednesday, February 02, 2005 10:33 AM  
To: Minnifield, Nita  
Subject: RE: sequence search request

Nita,

I apologize for the mix up. This query was searched against the AA dBS. Printing results now. Expect delivery by COB today.

Beverly

-----Original Message-----

From: Minnifield, Nita  
Sent: Tuesday, February 01, 2005 5:46 PM  
To: Shears, Beverly  
Subject: FW: sequence search request

Beverly,  
Please run a commercial and interference search on the amino acid sequence of SEQ ID NO:41 against the aa databases. If I am not making the proper request please let me know how I should it for future reference.

Thanks,  
Minnifield

-----Original Message-----

From: Minnifield, Nita  
Sent: Tuesday, January 11, 2005 9:51 AM  
To: STIC-Biotech/ChemLib  
Subject: sequence search request

STIC,

09/837344

Please do a commercial and interference  
sequence search on SEQ ID NO: 41 of this  
application.

1

Date completed: \_\_\_\_\_

Searcher: Beverly e 2528

Terminal time: \_\_\_\_\_

Elapsed time: \_\_\_\_\_

CPU time: \_\_\_\_\_

Total time: \_\_\_\_\_

Number of Searches: \_\_\_\_\_

Number of Databases: \_\_\_\_\_

Search Site

\_\_\_\_\_ STIC

\_\_\_\_\_ CM-1

\_\_\_\_\_ Pre-S

Type of Search

\_\_\_\_\_ N.A. Sequence

\_\_\_\_\_ A.A. Sequence

\_\_\_\_\_ Structure

\_\_\_\_\_ Bibliographic

Vendors--

\_\_\_\_\_ IG

\_\_\_\_\_ STN

\_\_\_\_\_ Dialog

\_\_\_\_\_ APS

\_\_\_\_\_ Geninfo

\_\_\_\_\_ SDC

\_\_\_\_\_ DARC/Questel

✓ Other CGN



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 4, 2005, 10:45:37 ; Search time 490.42 Seconds  
(without alignments)  
209.865 Million cell updates/sec

Title: US-09-837-344-31

Sequence: 1 SDLEGERAKERLQEQSDL.....GHLEKXGSIKPEQEDKS 316

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

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2: /cgn2\_6/ptodata/2/pubppaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubppaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB.pep.\*  
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9: /cgn2\_6/ptodata/2/pubppaa/US09A\_PUBCOMB.pep.\*  
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11: /cgn2\_6/ptodata/2/pubppaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubppaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubppaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubppaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubppaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubppaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubppaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1563	100.0	316 9 US-09-837-344-31	Sequence 31, Appl
2	1563	100.0	316 10 US-09-900-963-31	Sequence 31, Appl
3	603	38.6	117 9 US-09-837-344-20	Sequence 20, Appl
4	603	38.6	117 10 US-09-900-963-20	Sequence 20, Appl
5	554	35.4	107 9 US-09-837-344-19	Sequence 19, Appl
6	554	35.4	107 10 US-09-900-963-19	Sequence 19, Appl
7	329.5	21.1	1439 17 US-10-754-079-157	Sequence 157, Appl
8	329.5	21.1	1439 17 US-10-754-079-157	Sequence 157, Appl
9	327.5	21.0	1162 11 US-09-884-273-2	Sequence 2, Appl
10	326	20.9	611 9 US-09-284-804-2	Sequence 2, Appl
11	326	20.9	611 14 US-10-321-856-81	Sequence 81, Appl
12	320	20.5	350 13 US-10-101-487-58	Sequence 58, Appl
13	311	19.9	621 15 US-10-108-260A-4409	Sequence 4409, Ap

14	307	19.6	240 13 US-10-101-487-75	Sequence 75, Appl
15	288	18.4	650 15 US-10-104-047-3636	Sequence 3636, Ap
16	282	18.0	466 15 US-10-108-260A-4344	Sequence 4344, Ap
17	280.5	17.9	345 14 US-10-029-386-34255	Sequence 34255, A
18	278	17.8	280 15 US-10-104-047-3063	Sequence 3063, Ap
19	277	17.7	735 15 US-10-144-194A-109	Sequence 109, App
20	277	17.7	784 15 US-10-144-194A-108	Sequence 108, App
21	277	17.7	784 15 US-10-144-194A-84	Sequence 84, Appl
22	275	17.6	743 15 US-10-144-194A-86	Sequence 86, Appl
23	273	17.5	507 15 US-10-425-114-47285	Sequence 47285, A
24	273	17.5	696 15 US-10-424-599-196058	Sequence 196058,
25	272	17.4	1170 15 US-10-341-434-95	Sequence 95, Appl
26	272	17.4	1564 15 US-10-144-198-2	Sequence 2, Appl
27	272	17.4	1564 15 US-10-144-198-50	Sequence 4, Appl
28	268	17.1	187 13 US-10-101-487-50	Sequence 50, Appl
29	268	17.1	798 15 US-10-104-047-3335	Sequence 335, Ap
30	264	16.9	336 17 US-10-754-079-158	Sequence 158, App
31	261.5	16.7	1209 13 US-10-101-487-53	Sequence 53, Appl
32	261	16.7	179 13 US-10-101-487-46	Sequence 46, Appl
33	261	16.7	186 13 US-10-101-487-44	Sequence 44, Appl
34	261	16.7	191 13 US-10-101-487-81	Sequence 81, Appl
35	260.5	16.7	198 13 US-10-101-487-42	Sequence 42, Appl
36	260.5	16.7	287 14 US-10-029-386-33041	Sequence 33041, A
37	259.5	16.6	267 15 US-10-424-599-196057	Sequence 196057,
38	259	16.6	181 13 US-10-101-487-45	Sequence 45, Appl
39	258	16.5	197 13 US-10-101-487-70	Sequence 70, Appl
40	257	16.4	176 13 US-10-101-487-114	Sequence 114, Appl
41	256	16.4	177 13 US-10-101-487-48	Sequence 48, Appl
42	256	16.4	177 13 US-10-101-487-115	Sequence 115, Appl
43	255.5	16.3	501 15 US-10-335-977-8259	Sequence 8259, Ap
44	255.5	16.3	505 15 US-10-335-977-8260	Sequence 8260, Ap
45	255.5	16.3	1960 15 US-10-236-031B-62	Sequence 62, Appl

#### ALIGNMENTS

RESULT 1  
US-09-837-344-31  
Sequence 31, Application US/09837344  
Patent No. US20020041882A1  
GENERAL INFORMATION:  
APPLICANT: GUERIN-MARCHAND, Claudine  
DRUILHE, Pierre  
TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE  
HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE  
OF STIMULATING THE T LYMPHOCYTES  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/837,344  
FILING DATE: 19-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/462,625  
FILING DATE: <Unknown>  
APPLICATION NUMBER: FR 91 01286  
FILING DATE: 05-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McGowan, Malcolm K.  
REGISTRATION NUMBER: 39,300  
REFERENCE/DOCKET NUMBER: 010830-078

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 3, 2005, 11:23:14 ; Search time 42.3279 Seconds  
(without alignments)  
495.098 Million cell updates/sec

Title: US-09-837-344-31  
Perfect score: 1563

Sequence: 1 SDRGERAKRKLQGGQSDL.....GHLEKKGSGIKPEKEDKS 316

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1563	100.0	316	US-08-098-327E-31	Sequence 31, Appl
2	1563	100.0	316	US-08-462-625-31	Sequence 31, Appl
3	603	38.6	117	US-08-098-327E-20	Sequence 20, Appl
4	603	38.6	117	US-08-462-625-20	Sequence 20, Appl
5	554	35.4	107	US-08-098-327E-19	Sequence 19, Appl
6	344	22.0	608	US-09-270-767-32937	Sequence 19, Appl
7	344	22.0	608	US-09-270-767-48154	Sequence 32937, A
8	327.5	21.0	1162	US-08-728-323A-2	Sequence 48154, A
9	327.5	21.0	1162	US-09-298-568-2	Sequence 2, Appl
10	327.5	21.0	1162	US-09-410-399-2	Sequence 2, Appl
11	327.5	21.0	1162	US-09-894-273-2	Sequence 2, Appl
12	327.5	21.0	1162	US-09-216-393B-81	Sequence 81, Appl
13	326	20.9	611	US-08-056-200-94	Sequence 94, Appl
14	317.5	20.3	1898	US-08-800-644-94	Sequence 94, Appl
15	317.5	20.3	1898	US-09-538-092-1280	Sequence 1280, Ap
16	317.5	20.3	1898	US-09-543-681A-6436	Sequence 6436, Ap
17	301	19.3	1180	US-10-164-595-80	Sequence 80, Appl
18	277	17.7	784	US-10-164-595-79	Sequence 79, Appl
19	277	17.7	784	US-10-164-595-54	Sequence 54, Appl
20	275	17.6	779	US-09-270-767-44900	Sequence 56, Appl
21	265	17.0	676	US-09-248-796A-14503	Sequence 14503, A
22	260	16.6	613	US-09-543-681A-6012	Sequence 6012, Ap
23	259	16.6	613	US-09-538-092-1077	Sequence 1077, Ap
24	255	16.3	683	US-09-538-092-1077	Sequence 1077, Ap
25	255	16.3	683	US-09-538-092-1077	Sequence 1077, Ap
26	255	16.3	683	US-09-538-092-1077	Sequence 1077, Ap
27	253	16.2	2101	US-08-466-390-4	Sequence 4, Appl

28	253	16.2	2101	1	US-08-470-950-4	Sequence 4, Appl
29	253	16.2	2101	1	US-08-467-781-4	Sequence 4, Appl
30	253	16.2	2101	1	US-08-195-487-4	Sequence 4, Appl
31	253	16.2	2101	2	US-08-483-924-4	Sequence 1, Appl
32	253	16.2	2101	3	US-09-452-294-1	Sequence 4, Appl
33	253	16.2	2101	5	PCT-US93-06160-4	Sequence 4, Appl
34	250.5	16.0	1976	4	US-09-538-092-1078	Sequence 1078, Ap
35	247.5	15.8	1937	4	US-09-538-092-918	Sequence 918, Ap
36	247.5	15.8	1939	3	US-09-310-187A-1	Sequence 1, Appl
37	247.5	15.8	1939	4	US-09-538-092-917	Sequence 917, App
38	246	15.7	1972	4	US-08-875-435B-4	Sequence 4, Appl
39	245.5	15.7	1239	4	US-09-688-188B-13	Sequence 13, Appl
40	245.5	15.7	1239	4	US-09-291-417D-13	Sequence 13, Appl
41	245.5	15.7	1972	4	US-08-875-435B-3	Sequence 3, Appl
42	244.5	15.6	1866	3	US-08-938-105-3	Sequence 3, Appl
43	244	15.6	235	4	US-09-270-767-36681	Sequence 36681, A
44	244	15.6	235	4	US-09-270-767-51898	Sequence 51898, A
45	244	15.6	793	4	US-09-538-092-1271	Sequence 1271, Ap

## ALIGNMENTS

RESULT 1  
US-08-098-327E-31  
Sequence 31, Application US/08098327E

Patent No. 6270771

GENERAL INFORMATION:

APPLICANT: GUERIN-MARCHAND, Claudine

APPLICANT: DRULHE, Pierre

TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE

TITLE OF INVENTION: HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE

TITLE OF INVENTION: OF STIMULATING THE T LYMPHOCYTES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 2213-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/098,327E

FILING DATE: 24-NOV-1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 91 01286

FILING DATE: 05-FEB-1991

ATTORNEY/AGENT INFORMATION:

NAME: McGowan, Malcolm K.

REGISTRATION NUMBER: 39,300

REFERENCE/DOCKET NUMBER: 010830-045

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 316 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

PUBLICATION INFORMATION:

DOCUMENT NUMBER: WO 92/13884

PUBLICATION DATE: 20-AUG-1992

Query Match 100.0%, Score 1563, DB 3, Length 316;

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 3, 2005, 11:23:14 ; Search time 91.9518 seconds  
(without alignments)  
1232.776 Million cell updates/sec

Title: US-09-837-344-31

Sequence: 1 SLEGEERRAKERLQEQQSDL.....GHLEKXGSGIRPEKEDKS 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23sep04:\*  
1: geneeqp19808:\*  
2: geneeqp19908:\*  
3: geneeqp20008:\*  
4: geneeqp20018:\*  
5: geneeqp20028:\*  
6: geneeqp20038:\*  
7: geneeqp20038:\*  
8: geneeqp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1549	99.1	493	2 AAR26944	Aar26944 P.falcipa
3	942.5	60.3	462	2 AAR05766	Aar05766 Portion o
4	771.5	49.4	318	2 AAR26943	Aar26943 P.falcipa
5	739	47.3	456	8 ADO21942	Ado21942 LSA-NRC(H
6	739	47.3	457	8 ADO21942	Ado21942 LSA-NRC(H
7	603	38.6	117	2 AAR26937	Aar26937 P.falcipa
8	331	21.2	207	3 AAB44672	Aab44672 Gene 33 h
9	327.5	21.0	1162	3 AAY96255	Aay96255 Kaposi's
10	327.5	21.0	1162	3 AAY96255	Aay96255 Kaposi's
11	327.5	21.0	1162	3 AAB62331	Aab62331 Amino aci
12	327.5	21.0	1162	5 AAB05621	Aab05621 Kaposi's
13	327.5	21.0	1162	8 AAD65096	Ad65096 HHV8 late
14	326	20.9	611	4 AAU29039	Aau29039 T. gondii
15	326	20.9	611	4 AAU29039	Aau29039 T. gondii
16	326	20.9	611	4 AAU29039	Aau29039 T. gondii
17	321	20.5	360	2 AAM03627	Aam03627 Human fol
18	321	20.5	412	2 AAM03627	Aam03627 Human fol
19	321	20.5	554	4 ABB59454	Abb59454 Human thy
20	317.5	20.3	1898	7 AAY30795	Aay30795 Human tes
21	317.5	20.3	1898	7 AAY30795	Aay30795 Human tes
22	312	20.0	345	4 ABO05724	Ab005724 Human tes
23	311	19.9	621	7 ABB56557	Abb56557 Drosophi
24	306	19.6	2274	4 ABB56557	Abb56557 Drosophi
25	302.5	19.4	562	2 AAR70491	Aar70491 Leucocyto

26	301	19.3	1180	7 ADF06151	Adf06151 Bacterial
27	296.5	19.0	2990	8 ADP29884	Adp29884 Human sec
28	289	18.5	407	8 ADP49328	Adp49328 S pyrogen
29	289	18.5	923	4 ABG08600	Abg08600 Novel hum
30	288	18.4	650	7 ADB65482	Adb65482 Human pro
31	288	18.4	949	4 ABG15508	Abg15508 Novel hum
32	285	18.2	1940	8 ADP29883	Adp29883 Human sec
33	284	18.2	67	1 AAR81355	Aar81355 Sequence
34	284	18.2	1715	7 ABB58089	Abb58089 Drosophi
35	282	18.0	466	7 ADM05659	Adm05659 Human pro
36	281	18.0	800	4 ABB65632	Abb65632 Drosophi
37	281	18.0	800	4 ABB71459	Abb71459 Drosophi
38	280.5	17.9	345	8 ABO60621	Ab060621 Human gen
39	278	17.8	280	7 ADB64909	Adb64909 Human pro
40	277	17.7	695	4 AAM79466	Aam79466 Human pro
41	277	17.7	735	6 ABR58340	Ab58340 AAC97961
42	277	17.7	735	6 ABR58340	Ab58340 Angiogene
43	277	17.7	784	6 ABR58339	Ab58339 AAF19255
44	277	17.7	784	6 ABO52982	Ab052982 Human put
45	277	17.7	784	7 ADB65840	Adb65840 Angiogene

## ALIGNMENTS

## RESULT 1

AAR26941 ID AAR26941 standard; protein; 316 AA.

XX AAR26941;

AC 25-MAR-2003 (revised)  
DT 08-FEB-1993 (first entry)

XX P.falciparum LSA-R-NR protein.

KW Malaria; hepatocyte; sporozoite; plasmid DG 536; T-cell epitope;  
KW palindrom; liver stage-specific antigen.

XX Plasmodium falciparum.

OS Plasmodium falciparum.

XX Key Location/Qualifiers  
FH 1..209  
FT /label= repeat\_region  
FT /note= "contains 12 x 17mer repeats"  
FT 210..316  
FT /label= non-repeat\_region

XX Region  
XX MO9213884-A1.

XX 20-AUG-1992.

XX 05-FEB-1992; 92WO-FR000104.

XX 05-FEB-1991; 91FR-00001286.

XX (INSP) INST PASTEUR.

XX Guerimarchand C, Drulhe P;

XX WPI; 1992-299985/36.

XX N-PSDB; AAQ28115.

XX Polypeptide(s) derived from liver stage of PLASMODIUM FALCIPARUM - for  
XX vaccination against, treatment of and diagnosis of malaria.

XX Disclosure; Fig 1; 81pp; French.

XX A genomic DNA bank of P.falciparum EcoRI fragments prepared in lambda  
XX gtl1 was used to transform E.coli. The expression library was screened  
XX with human antisera against antigens of all stages of P. falciparum. The  
XX library was rescreened with antibodies affinity-purified on a clone  
XX which was able to recognise antibodies specific to the hepatic phase.

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 3, 2005, 11:23:14 ; Search time 33.5058 Seconds

(without alignments)  
2009.171 Million cell updates/sec

Title: US-09-837-344-20

Sequence: 1 LQEQRDLEGRKADTKKQLE.....GHLEKKDGSIKPEQKEDKS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : uniprot\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	603	100.0	493	2	Q25886
2	602	99.8	1909	2	Q25893
3	597	99.0	1596	2	Q25844
4	554	91.9	280	2	Q25844
5	554	91.9	280	2	Q25849
6	554	91.9	280	2	Q25850
7	553	91.7	280	2	Q25843
8	553	91.7	280	2	Q25846
9	553	91.7	280	2	Q25847
10	553	91.7	280	2	Q25851
11	550	91.2	280	2	Q25848
12	550	91.2	280	2	Q25852
13	549	91.0	280	2	Q25845
14	549	91.0	280	2	Q25853
15	549	91.0	280	2	Q25854
16	549	91.0	280	2	Q25855
17	549	91.0	280	2	Q25888
18	549	91.0	280	2	Q25889
19	549	91.0	280	2	Q25900
20	549	91.0	280	2	Q27243
21	469	77.8	264	2	Q25843
22	224	37.1	42	2	Q25843
23	102	16.9	210	2	Q25843
24	98.5	16.3	924	2	Q25843
25	94.5	15.7	772	2	Q25843
26	92	15.3	603	2	Q25843
27	91.5	15.2	635	2	Q25843
28	91	15.1	294	2	Q25843
29	90.5	15.0	1085	2	Q25843
30	90	14.9	225	2	Q25843
31	90	14.9	756	1	EFER_HUMAN

32	89.5	14.8	295	2	Q6BXX9	Q6BXX9
33	89.5	14.8	485	2	Q7SEU2	Q7SEU2
34	89.5	14.8	485	2	AA550359	AA550359
35	89.5	14.8	6328	2	Q8MNS0	Q8MNS0
36	89.5	14.8	18519	2	Q8ISF6	Q8ISF6
37	89.5	14.8	18534	2	Q8ISF7	Q8ISF7
38	88	14.6	217	2	Q6QTF7	Q6QTF7
39	88	14.6	217	2	AA517876	AA517876
40	88	14.6	710	2	Q7RJNS	Q7RJNS
41	88	14.6	791	2	Q22142	Q22142
42	87.5	14.5	262	1	NSB1_HUMAN	Q22142
43	87.5	14.5	1418	2	Q86HT4	Q86HT4
44	87	14.4	535	2	Q44192	Q44192
45	87	14.4	650	2	Q7RCN9	Q7RCN9

## ALIGNMENTS

RESULT 1	Q25886	PRELIMINARY;	PRT;	493 AA.
ID	Q25886			
AC	Q25886			
DT	01-NOV-1996	(TRENBLREL. 01, Created)		
DT	01-NOV-1996	(TRENBLREL. 01, Last sequence update)		
DE	01-OCT-2002	(TRENBLREL. 22, Last annotation update)		
DE	Liver stage antigen-1 (Fragment).			
GN	Name=LSA-1;			
OS	Plasmodium falciparum.			
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.			
OX	NCBI_TaxID=5833;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94267224; PubMed=7515922;			
RA	Fidock D.A., Grais-Masse H., Lepeux J., Brahimi K., Benmohamed L.,			
RA	Mellouk S., Guerin-Marchand C., Londono A., Raharimalala L.,			
RA	Meis J.F., Langsley G., Roussillon C., Tartar A., Drulhe P.,			
RT	"Plasmodium falciparum liver stage antigen-1 is well conserved and			
RT	contains potent B and T cell determinants."			
RL	J. Immunol. 153:190-204(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Fidock D.A., Grais-Masse H., Lepeux J., Brahimi K., Benmohamed L.,			
RA	Mellouk S., Guerin-Marchand C., Londono A., Raharimalala L.,			
RA	Meis J.F., Langsley G., Roussillon C., Tartar A., Drulhe P.,			
RT	"The Plasmodium falciparum liver stage antigen LSA-1 is well conserved			
RT	and harbors major B- and T-cell epitopes."			
DR	EMBL, Z30320; CAA82975.1; -.			
FT	NON-TER			
SC	SEQUENCE 493 AA; 59062 MW; PE252C44F46996E CRC64;			
Query Match	100.0%; Score 603; DB 2; Length 493;			
Best Local Similarity	100.0%; Pred. No. 2, 8e-42;			
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	LQEQRDLEGRKADTKKLEKKGDIILAEVIGRLIEPAIEPSNENRGYYPHOSL 60		
Db	204	LQEQRDLEGRKADTKKLEKKGDIILAEVIGRLIEPAIEPSNENRGYYPHOSL 263		
Qy	61	PDNRGNSRDSKEISIEKTNRRESITTVNVEGRDINHGHLEKKDGSIKPEQKEDKS 117		
Db	264	PDNRGNSRDSKEISIEKTNRRESITTVNVEGRDINHGHLEKKDGSIKPEQKEDKS 320		
RESULT 2	Q25893	PRELIMINARY;	PRT;	1909 AA.
ID	Q25893			
AC	Q25893			
DT	01-NOV-1996	(TRENBLREL. 01, Created)		
DT	01-NOV-1996	(TRENBLREL. 01, Last sequence update)		
DT	01-JUN-2003	(TRENBLREL. 24, Last annotation update)		
DE	Liver stage antigen.			

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OM protein - protein search, using sw model

Run on: February 3, 2005, 11:23:13 ; Search time 14.0508 Seconds  
(without alignments)  
801.190 Million cell updates/sec

Title: US-09-837-344-20

Sequence: 1 LQEQORDLEQRKADTKNLE.....GHLEEKQGSIKPEQEKDPS 117

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	602	99.8	1909	2 A45592	liver stage antigen
2	102	16.9	210	2 C70309	transcription regu
3	94.5	15.7	772	2 I50463	protein kinase - c
4	91.5	15.2	635	1 I37060	involucrin L - gor
5	90.5	15.0	1085	2 S53352	IFM1 protein - yea
6	90	14.9	756	2 T00367	hypothetical prote
7	89.5	14.8	3488	2 T34418	hypothetical prote
8	88	14.6	762	2 G88436	protein T04A.13 l
9	87	14.6	791	2 T24335	hypothetical prote
10	87	14.4	550	2 T23560	hypothetical prote
11	87	14.4	779	2 E34024	hypothetical prote
12	84.5	14.0	585	1 A24168	protein kinase (EC
13	84.5	14.0	605	1 I37061	involucrin - human
14	84.5	14.0	765	1 ISHUT1	involucrin M - gor
15	84	13.9	913	2 T52485	DNA topoisomerase
16	83.5	13.8	615	2 T06108	neurofilament prot
17	83.5	13.8	789	2 T51310	hypothetical prote
18	83.5	13.8	821	2 S67087	RNA helicase RH28
19	83.5	13.8	1025	2 A47453	hypothetical prote
20	83.5	13.8	1706	2 T29305	transcription fact
21	83	13.8	483	2 S41853	protein kinase - f
22	83	13.8	684	2 S52835	centromere/microtu
23	82.5	13.7	495	1 I37062	hypothetical prote
24	82.5	13.7	1027	2 S37711	involucrin S - gor
25	81.5	13.5	442	2 D70315	kinesin heavy chai
26	81.5	13.5	980	2 E71606	transcription regu
27	81.5	13.5	1829	2 T26135	hypothetical prote
28	81	13.4	543	2 T32973	hypothetical prote
29	81	13.4	1390	2 T14004	cyta protein - sll

30	80.5	13.3	678	2 A54514	glutamic acid-rich
31	80.5	13.3	768	2 H54024	protein kinase (EC
32	80.5	13.3	777	2 B54024	protein kinase (EC
33	80.5	13.3	1032	2 T34510	neutonal kinesin h
34	80.5	13.3	1804	2 T34518	neutrin - golden ha
35	80	13.3	452	2 D64583	hypothetical prote
36	80	13.3	729	2 T50989	hypothetical prote
37	79.5	13.2	501	2 C71948	hypothetical prote
38	79.5	13.2	816	2 S64439	hypothetical prote
39	79.5	13.2	1132	2 T43483	hypothetical prote
40	79.5	13.2	1203	2 S26650	translation initia
41	79.5	13.2	1840	2 T29091	DNA-binding protei
42	79	13.1	511	2 H83339	transactin - chic
43	79	13.1	630	2 S29796	probable transcrip
44	79	13.1	721	2 S29796	hypothetical prote
45	79	13.1	783	2 A55817	hypothetical prote
					cyclin-dependent k

## ALIGNMENTS

RESULT 1  
A45592  
liver stage antigen LSA-1 - malaria parasite (Plasmodium falciparum)  
C:Species: Plasmodium falciparum  
C:Date: 22-Nov-1993 #sequence\_revision 02-Dec-1994 #text\_change 09-Jul-2004  
C:Accession: S24597; A45592; S29393; S34842; B45592; C45592; D45592  
R:Zhu, J.; Hollingdale, M.  
Submitted to the EMBL Data Library, November 1990  
A:Reference number: S24597  
A:Accession: S24597  
A:Molecule type: DNA  
A:Residues: 1-1909 <ZHU>  
A:Cross-references: UNIPROT:Q25893; EMBL:X56203; NID:93915; PID:93916  
R:Zhu, J.; Hollingdale, M.R.  
Mol. Biochem. Parasitol. 48, 223-226, 1991  
A:Title: Structure of Plasmodium falciparum liver stage antigen-1.  
A:Reference number: A45592; MUID:92107224; PMID:1840628  
A:Accession: A45592  
A:Molecule type: DNA  
A:Residues: 1-195;638-688;1165-1215;1590-1909 <ZH2>  
A:Note: sequence extracted from NCBI backbone (NCBIN:75010, NCBIN:75012, NCBIN:75014, X  
R:Guerin-Marchand, C.; Druilhe, P.; Galey, B.; Londono, A.; Pataportikul, J.; Beaudoir  
Nature 329, 164-167, 1987  
A:Title: A liver-stage-specific antigen of Plasmodium falciparum characterized by gene  
A:Reference number: S29393; MUID:87315391; PMID:3306406  
A:Accession: S29393  
A:Molecule type: DNA  
A:Status: preliminary  
A:Residues: 323-387 <GUE1>  
A:Cross-references: EMBL:M28266  
R:Guerin-Marchand, C.; Druilhe, P.; Galey, B.; Londono, A.; Pataportikul, J.; Beaudoir  
Submitted to the EMBL Data Library, April 1992  
A:Description: a liver-stage-specific antigen of plasmodium falciparum characterized by  
A:Reference number: S34842  
A:Accession: S34842  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 323-381, 'HKA1' <GUE2>  
A:Cross-references: EMBL:M28266  
A:Note: difference at carboxyl end due to frameshift error  
C:Comment: This protein is found as flocculent material in the parasitophorous vacuole.  
C:Superfamily: trichonyalin calmodulin repeat homology  
C:Keywords: EF hand  
F:154-1629/Region: 17-residue repeats (A-K-E-K-L-Q-E-Q-S-D-L-E-Q-E-R-R)  
Query Match 99.8%; Score 602; DB 2; Length 1909;  
Best Local Similarity 99.1%; Pred. No. 2.2e+43;  
Matches 116; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQEQORDLEQRKADTKNLEKKGDI LAEDLYGRLEIPALISPSENERGYIIPHOSSL 60  
DB 1620 LQEQORDLEQRKADTKNLEKKGHDVLAEDLYGRLEIPALISPSENERGYIIPHOSSL 1679



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OM protein - protein search, using sw model

Run on: February 4, 2005, 10:45:37 ; Search time 181.58 Seconds  
(without alignments)  
209.865 Million cell updates/sec

Title: US-09-837-344-20

Perfect score: 603  
Sequence: 1 LQEQQRDLQKRAVDKKNLE.....GHLEKKGDSIKPEQKEDKS 117

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
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- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
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- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	603	100.0	117	9	US-09-837-344-20
2	603	100.0	117	9	US-09-900-963-20
3	603	100.0	316	9	US-09-837-344-31
4	603	100.0	316	10	US-09-900-963-31
5	554	91.9	107	9	US-09-837-344-19
6	554	91.9	107	10	US-09-900-963-19
7	154	25.5	31	9	US-09-837-344-23
8	154	25.5	31	10	US-09-900-963-23
9	141	23.4	27	9	US-09-837-344-21
10	141	23.4	27	10	US-09-900-963-21
11	94	15.6	456	9	US-09-894-018-121
12	89.5	14.8	231	9	US-09-922-261-194
13	89.5	14.8	232	9	US-09-922-261-192

14	89.5	14.8	238	9	US-09-922-261-190	Sequence 190, App
15	89.5	14.8	257	9	US-09-922-261-188	Sequence 188, App
16	89.5	14.8	272	9	US-09-922-261-186	Sequence 186, App
17	87	14.4	550	15	US-10-369-493-5995	Sequence 5995, Ap
18	85.5	14.2	765	10	US-09-882-274-2	Sequence 2, Appl
19	85.5	14.2	765	16	US-10-408-765A-1149	Sequence 1149, Ap
20	85	14.1	15	13	US-10-103-395-74	Sequence 74, Appl
21	84	13.9	24	9	US-09-837-344-22	Sequence 22, Appl
22	84	13.9	24	10	US-09-900-963-22	Sequence 22, Appl
23	83.5	13.8	257	15	US-10-425-114-58860	Sequence 58860, A
24	83.5	13.8	395	15	US-10-425-114-59744	Sequence 69744, A
25	83.5	13.8	903	15	US-10-282-122A-52328	Sequence 52328, A
26	83	13.8	2683	16	US-10-437-663-185370	Sequence 185370, A
27	82.5	13.7	1027	14	US-10-080-608A-27	Sequence 27, Appl
28	82.5	13.7	1027	15	US-10-370-685-116	Sequence 116, App
29	82.5	13.7	1264	15	US-10-369-493-3742	Sequence 3742, Ap
30	82	13.6	472	10	US-09-953-407-2	Sequence 2, Appl
31	82	13.6	1429	10	US-09-953-407-1	Sequence 1, Appl
32	81.5	13.5	485	10	US-09-769-736-72	Sequence 72, Appl
33	81	13.4	294	15	US-10-425-114-49118	Sequence 49118, A
34	81	13.4	396	15	US-10-424-599-168151	Sequence 168151, A
35	81	13.4	542	15	US-10-424-599-234091	Sequence 234091, A
36	80.5	13.3	1032	14	US-10-080-608A-26	Sequence 26, Appl
37	80.5	13.3	1032	15	US-10-370-685-115	Sequence 115, App
38	80	13.3	452	9	US-09-881-752A-268	Sequence 268, App
39	80	13.3	452	15	US-10-282-122A-58723	Sequence 58723, A
40	79.5	13.2	321	9	US-09-864-761-33718	Sequence 33718, A
41	79.5	13.2	361	9	US-09-864-761-33614	Sequence 33614, A
42	79.5	13.2	361	9	US-09-864-761-34141	Sequence 34141, A
43	79.5	13.2	501	15	US-10-335-977-8259	Sequence 8259, Ap
44	79.5	13.2	505	15	US-10-335-977-8260	Sequence 8260, Ap
45	79.5	13.2	886	15	US-10-260-708-66	Sequence 66, Appl

## ALIGNMENTS

RESULT 1  
US-09-837-344-20  
Sequence 20, Application US/09837344  
Patent No. US20020041882A1

GENERAL INFORMATION:  
APPLICANT: GUERIN-MARCHAND, Claudine  
DRUILHE, Pierre  
TITLE OF INVENTION: HEPATIC SEQUENCES SPECIFIC FOR THE  
HEPATITIS STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE  
OF STIMULATING THE T LYMPHOCYTES

NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/837,344  
FILING DATE: 19-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/462,625  
FILING DATE: <Unknown>  
APPLICATION NUMBER: FR 91 01286  
FILING DATE: 05-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McGowan, Malcolm K.  
REGISTRATION NUMBER: 39,300  
REFERENCE/DOCKET NUMBER: 010830-078

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OM protein - protein search, using sw model

Run on: February 3, 2005, 11:23:14 ; Search time 15.6721 Seconds  
(without alignments)  
495.098 Million cell updates/sec

Title: US-09-837-344-20

Perfect score: 603  
1 LGEQRDLGRKADTKKLE.....GHLEKKDSIKPEKEDKS 117

Scoring table: BLOSUM62

Searched: 478139 seqs, 66318000 residues  
Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/prodata/1/1aa/5A COMB.pep.\*  
2: /cgn2\_6/prodata/1/1aa/5B COMB.pep.\*  
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4: /cgn2\_6/prodata/1/1aa/6B COMB.pep.\*  
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6: /cgn2\_6/prodata/1/1aa/backfillsl.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	603	100.0	117	3	US-08-098-327E-20
2	603	100.0	117	3	US-08-462-625-20
3	603	100.0	316	3	US-08-098-327E-31
4	603	100.0	316	3	US-08-462-625-31
5	554	91.9	107	3	US-08-098-327E-19
6	554	91.9	107	3	US-08-462-625-19
7	154	25.5	31	3	US-08-098-327E-23
8	154	25.5	31	3	US-08-462-625-23
9	141	23.4	27	3	US-08-098-327E-21
10	141	23.4	27	3	US-08-462-625-21
11	97	16.1	709	4	US-09-248-796A-19045
12	90.5	15.0	1085	1	US-08-431-080-28
13	90.5	15.0	1085	2	US-08-538-534-28
14	90.5	15.0	1085	2	US-09-345-294-28
15	89.5	14.8	231	3	US-09-461-697-194
16	89.5	14.8	232	3	US-09-461-697-192
17	89.5	14.8	238	3	US-09-461-697-190
18	89.5	14.8	257	3	US-09-461-697-188
19	89.5	14.8	272	3	US-09-461-697-186
20	86	14.3	447	4	US-09-710-279-2900
21	86	14.3	450	4	US-09-710-279-3226
22	85.5	14.2	765	4	US-09-538-092-906
23	85	14.1	15	4	US-09-009-953-74
24	84.5	14.0	150	3	US-09-395-689-2
25	84.5	14.0	300	3	US-09-395-689-1
26	84.5	14.0	765	2	US-08-663-112-2
27	84	13.9	24	3	US-08-098-327E-22

28	84	13.9	24	3	US-08-462-625-22	Sequence 22, Appl.
29	84	13.9	1761	4	US-09-561-709B-1	Sequence 1, Appl
30	83.5	13.8	1025	4	US-09-538-092-334	Sequence 334, App
31	82.5	13.7	1027	4	US-09-914-259-27	Sequence 27, Appl
32	80.5	13.3	129	4	US-09-513-999C-5707	Sequence 5707, Ap
33	80.5	13.3	1032	4	US-09-914-259-26	Sequence 26, Appl
34	80.5	13.3	1032	4	US-09-538-092-1293	Sequence 1293, Ap
35	79	13.1	140	4	US-09-710-279-2288	Sequence 2288, Ap
36	79	13.1	140	4	US-09-710-279-2288	Sequence 2438, Ap
37	79	13.1	147	3	US-09-134-001C-5518	Sequence 5518, Ap
38	79	13.1	538	4	US-09-252-991A-23551	Sequence 23551, A
39	79	13.1	708	3	US-08-235-836C-76	Sequence 76, Appl
40	78	12.9	452	4	US-09-538-092-14553	Sequence 14553, A
41	78	12.9	1270	4	US-09-543-681A-6752	Sequence 1321, Ap
42	77.5	12.9	474	4	US-08-235-836C-72	Sequence 6752, Ap
43	77.5	12.9	693	3	US-08-235-836C-72	Sequence 72, Appl
44	77.5	12.9	785	4	US-09-248-796A-24492	Sequence 24492, A
45	77	12.8	422	4	US-09-248-796A-19321	Sequence 19321, A

## ALIGNMENTS

RESULT 1  
US-08-098-327E-20  
Sequence 20, Application US/08098327E  
Patent No. 6270771  
GENERAL INFORMATION:  
APPLICANT: GUERIN-MARCHAND, Claudine  
TITLE OF INVENTION: DRUGS, Peptide  
TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE  
HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE  
OF STIMULATING THE T LYMPHOCYTES  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Burns, Doane, Swecker & Machis  
STREET: P. O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/098,327E  
FILING DATE: 24-NOV-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 01286  
FILING DATE: 05-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McGowan, Malcolm K.  
REGISTRATION NUMBER: 39,300  
REFERENCE/DOCKET NUMBER: 010830-045  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PUBLICATION INFORMATION:  
DOCUMENT NUMBER: WO 92/13884  
PUBLICATION DATE: 20-AUG-1992  
US-08-098-327E-20  
Query Match 100.0%; Score 603; DB 3; Length 117;

